

KW

PCT09

RAW SEQUENCE LISTING DATE: 08/01/2001  
PATENT APPLICATION: US/09/763,535 TIME: 18:42:56

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\08012001\1763535.raw

4 <110> APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN  
5 ROUSSEAU, GUY  
6 LEMAIGRE, FREDRIC  
8 <120> TITLE OF INVENTION: PHARMACEUTICLA COMPOSITION FOR TREATING  
9 OR PREVENTING DIABETES OR CANCER, OR THE WAARDENBURG  
10 SYNDROME  
12 <130> FILE REFERENCE: DECLE26.001APC  
14 <140> CURRENT APPLICATION NUMBER: US 09/763,535  
15 <141> CURRENT FILING DATE: 2001-02-20  
17 <150> PRIOR APPLICATION NUMBER: BE 9800609  
18 <151> PRIOR FILING DATE: 1998-08-17  
20 <160> NUMBER OF SEQ ID NOS: 4  
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 1655  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Homo sapiens  
29 <400> SEQUENCE: 1  
30 gcccccgccc gccccgggcc ctgatggact gaatgaaggc tgcc tacacc gcctatcgat 60  
31 gcctcacc aa agacctagaa cgtgcgcatt gaacccggag ctgacaatgg aaagtctggg 120  
32 cacttgcac ggcgcgcgc ggcgcggcag tggcggggc ggcggcgggg gccgcgggg 180  
33 cggcggcggg ggcccgccg atgagcagg a gctgtggcc agcccccagcc cccaccacgc 240  
34 ggcgcgcggc cgcgtggct cgctgcggg ccctccggc ccttcaaccg cgcaccagg 300  
35 gctgggcacg gccgcaggcg cggcagcggc ggcgtgcgc tcggccatgg tcaccaggat 360  
36 ggcctcgatc ctggacggcg ggcactaccg gcccggatcc tccatcccgcc tgcaccacgc 420  
37 catgagcatg tcctgcgact cgctccggcc tggcatgggc atgagcaaca cttacaccac 480  
38 gctgacaccg ctccagccgc tgccacccat ctccaccgtg tctgacaagt tccaccaccc 540  
39 tcacccgcac caccatccgc accaccacca ccaccaccac caccaggcgc tgcaccaccc 600  
40 cgtcagcggc agttcaccc tcatgcgcga cggcgcggg ctccggccca tgaacaacct 660  
41 ctacagtccc tacaaggaga tgccggcat gagccagagc ctgtcccgcc tggccggccac 720  
42 gccgctggc aacgggctag ggcgcctcca caacgcgcag cagagtctgc ccaactacgg 780  
43 tccggcggc cacgacaaaaa tgctcagccc caacttcgac ggcaccaca ctgccatgct 840  
44 gaccggcggt gagcaacacc tggccggcgg cttggcacc ccacccgcgg ccatgatgtc 900  
45 gcacctgaac ggcgtgcacc accgggcca cactcagtct cacgggccc tgcgtggcacc 960  
46 cagtcgcgag cggccaccct cgtcctcatc gggctcgag gtggccacgt cggccagct 1020  
47 ggaagaaaatc aacaccaaaag aggtggccca ggcgcacatca gggagctga agcgctacag 1080  
48 tatccccca ggcgcacatcc tgcgcgggt gctgtggcc ttcaggggat ctctctccga 1140  
49 cctgtccgg aatccaaaac cgtggagtaa actcaaatct ggcaggagaa cttccgcag 1200  
50 gatgtggaa tggcttcagg agcccgagtt ccagcgcatg tccgccttac gcctggcagc 1260  
51 gtgcaaaacgc aaagagcaag aaccaaaacaa agacagggaa aattcccgaa agaagttccg 1320  
52 cctgggttcc actgacccctc aacggcgaac actttcgcc atcttcaagg agaacaacgc 1380  
53 cccgtcaag gagatgcaga tcaccattc ccagcagctg ggcctggagc tcacaaccgt 1440  
54 cagcaacttc ttcatgaacg cccggcgcgc ggcgcggag aagtggcaag acgatctgag 1500  
55 cacagggggc tcctcgatcc cttccagcac gtgtacccaa gcatgatgtga aggactctca 1560  
56 cttgggcaca agtcacccctc aaatgaggac aacagatacc aaaagaaaaac aaaggaaaa 1620  
57 gacaccggat tccttagctgg ggccttcac tggtg 1655  
59 <210> SEQ ID NO: 2

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60 <211> LENGTH: 485  
61 <212> TYPE: PRT  
62 <213> ORGANISM: Homo sapiens  
64 <400> SEQUENCE: 2  
65 Met Asn Pro Glu Leu Thr Met Glu Ser Leu Gly Thr Leu His Gly Ala  
66 1 5 10 15  
67 Arg Gly Gly Gly Ser Gly  
68 20 25 30  
69 Gly Gly Gly Pro Gly His Glu Gln Glu Leu Leu Ala Ser Pro Ser Pro  
70 35 40 45  
71 His His Ala Arg Arg Gly Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro  
72 50 55 60  
73 Pro Pro Thr Ala His Gln Glu Leu Gly Thr Ala Ala Ala Ala Ala  
74 65 70 75 80  
75 Ala Ala Ser Arg Ser Ala Met Val Thr Ser Met Ala Ser Ile Leu Asp  
76 85 90 95  
77 Gly Gly Asp Tyr Arg Pro Glu Leu Ser Ile Pro Leu His His Ala Met  
78 100 105 110  
79 Ser Met Ser Cys Asp Ser Ser Pro Pro Gly Met Gly Met Ser Asn Thr  
80 115 120 125  
81 Tyr Thr Thr Leu Thr Pro Leu Gln Pro Leu Pro Pro Ile Ser Thr Val  
82 130 135 140  
83 Ser Asp Lys Phe His His Pro His Pro His His His Pro His His His  
84 145 150 155 160  
85 His His His His Gln Arg Leu Ser Gly Asn Val Ser Gly Ser Phe  
86 165 170 175  
87 Thr Leu Met Arg Asp Glu Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr  
88 180 185 190  
89 Ser Pro Tyr Lys Glu Met Pro Gly Met Ser Gln Ser Leu Ser Pro Leu  
90 195 200 205  
91 Ala Ala Thr Pro Leu Gly Asn Gly Leu Gly Gly Leu His Asn Ala Gln  
92 210 215 220  
93 Gln Ser Leu Pro Asn Tyr Gly Pro Pro Gly His Asp Lys Met Leu Ser  
94 225 230 235 240  
95 Pro Asn Phe Asp Ala His His Thr Ala Met Leu Thr Arg Gly Glu Gln  
96 245 250 255  
97 His Leu Ser Arg Gly Leu Gly Thr Pro Pro Ala Ala Met Met Ser His  
98 260 265 270  
99 Leu Asn Gly Leu His His Pro Gly His Thr Gln Ser His Gly Pro Val  
100 275 280 285  
101 Leu Ala Pro Ser Arg Glu Arg Pro Pro Ser Ser Ser Gly Ser Gln  
102 290 295 300  
103 Val Ala Thr Ser Gly Gln Leu Glu Glu Ile Asn Thr Lys Glu Val Ala  
104 305 310 315 320  
105 Gln Arg Ile Thr Ala Glu Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile  
106 325 330 335  
107 Phe Ala Gln Arg Val Leu Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu  
108 340 345 350  
109 Leu Arg Asn Pro Lys Pro Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr

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110 355 360 365  
 111 Phe Arg Arg Met Trp Lys Trp Leu Gln Glu Pro Glu Phe Gln Arg Met  
 112 370 375 380  
 113 Ser Ala Leu Arg Leu Ala Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn  
 114 385 390 395 400  
 115 Lys Asp Arg Asn Asn Ser Gln Lys Lys Ser Arg Leu Val Phe Thr Asp  
 116 405 410 415  
 117 Leu Gln Arg Arg Thr Leu Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro  
 118 420 425 430  
 119 Ser Lys Glu Met Gln Ile Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu  
 120 435 440 445  
 121 Thr Thr Val Ser Asn Phe Phe Met Asn Ala Arg Arg Ser Leu Glu  
 122 450 455 460  
 123 Lys Trp Gln Asp Asp Leu Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser  
 124 465 470 475 480  
 125 Thr Cys Thr Lys Ala  
 126 485  
 129 <210> SEQ ID NO: 3  
 130 <211> LENGTH: 1485  
 131 <212> TYPE: DNA  
 132 <213> ORGANISM: Homo sapiens  
 134 <400> SEQUENCE: 3  
 135 atggagctga gcctggagag cctggggggc ctgcacagcg tggcccacgc gcaggcgggc 60  
 136 gagctgtga gccccggcca cgcgcgtctcg gggcgccgcg agcaccgcgg cctgggtggcg 120  
 137 cccggggcgc cggggctggc ggcggcatg gcgagcctgc tggacggcg cggcgccgc 180  
 138 ggcgggtggg ggcggggggg cgcggggcgcg gcgccgcgcg cggcgccgcg cgcggacttc 240  
 139 cgcgggaaac tggcgccccc gtcgcacccg gcaatggca tggcctgcga ggcgcgggc 300  
 140 ctgggcggca cctacacgac gtcacacccc ctgcagcacc tggcggccgtc cgcggccgtg 360  
 141 gccgacaagt tccaccagca cgcggcgccg gcgccgtgg cgggggcgc cggcgccat 420  
 142 ccccacgcgc acccgacccc ggcggccgcg cgcgcgcgc caccggccgc gcaacgtctg 480  
 143 gcggccagcg tgagcggcag cttcacccctc atgcgcgcacg agcggccgc gctgcctcc 540  
 144 gtggggccacc tctacggacc ctacggcaag gagctgccc ccatgggtc gccgctgtcg 600  
 145 ccgctgcca acgcgtgcc gcccgcgtc cacggccccc cgcagccccc gccgcgcaca 660  
 146 ccaccccccgc cgctggccgc ctacggcccg ccagggcacc tggctggga caagctgtcg 720  
 147 cccggccccc cttcgagcc gacgcgcgcg ctgcgtggac gcgcggagga cgcactggcc 780  
 148 cgcgggtgtc cgggaggcgg cggcgccaca ggcagcggcg gagcgggcag cggagcgc 840  
 149 gcggggctgc tggcgccgt gggcggtgt gcggcgccgc gggcgacgg gcccacggg 900  
 150 ggaggcgccg gccccggcgg gagcggcgcc ggcgcgcgc cggcgccgc ggcgcaggag 960  
 151 atcaacacca aggagggtggc gcagcgcata acggcgaggc tgaagcgcta cagcatcccg 1020  
 152 caggcaatct tgcgcgcagcg gatccctgtgt cgctctcagg gcacgcgtc cgcacgtctg 1080  
 153 cgcaacccca agccgtggag caagctaaa tccggccgcg agacctccg cagatgtgg 1140  
 154 aagtggctgc aggagccaga gttccagcgc atgtcgccgc tgcgttgc agcgtcaag 1200  
 155 cgcaaggaac aggagcagca gaaggagcgc gcccgcgc ccaagaagca gccgcgtgt 1260  
 156 ttcaccgacc tgcagcgcagc cacgtgtat gccatcttca aggagaacaa gccgcgtcc 1320  
 157 aaggagatgc aggtcaccat ctcgcagcag ctcggcttgg agctcaacac cgtcagcaac 1380  
 158 ttcttcatga acgcgcggcg ccgctgcata aaccgcgtgg ctgaggagcc cagcacggcc 1440  
 159 cccggggggc cgcggccgcg cacggccact ttctccaagg cctga 1485  
 161 <210> SEQ ID NO: 4  
 162 <211> LENGTH: 494

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163 <212> TYPE: PRT  
164 <213> ORGANISM: Homo sapiens  
166 <400> SEQUENCE: 4  
167 Met Glu Leu Ser Leu Glu Ser Leu Gly Gly Leu His Ser Val Ala His  
168 1 5 10 15  
169 Ala Gln Ala Gly Glu Leu Leu Ser Pro Gly His Ala Arg Ser Ala Ala  
170 20 25 30  
171 Ala Gln His Arg Gly Leu Val Ala Pro Gly Arg Pro Gly Leu Val Ala  
172 35 40 45  
173 Gly Met Ala Ser Leu Leu Asp Gly Gly Gly Gly Gly Gly Gly Gly  
174 50 55 60  
175 Ala Gly Gly Ala Gly Gly Ala Gly Ser Ala Gly Gly Gly Ala Asp Phe  
176 65 70 75 80  
177 Arg Gly Glu Leu Ala Gly Pro Leu His Pro Ala Met Gly Met Ala Cys  
178 85 90 95  
179 Glu Ala Pro Gly Leu Gly Gly Thr Tyr Thr Leu Thr Pro Leu Gln  
180 100 105 110  
181 His Leu Pro Pro Leu Ala Ala Val Ala Asp Lys Phe His Gln His Ala  
182 115 120 125  
183 Ala Ala Ala Ala Val Ala Gly Ala His Gly Gly His Pro His Ala His  
184 130 135 140  
185 Pro His Pro Ala Ala Ala Pro Pro Pro Pro Pro Pro Pro Gln Arg Leu  
186 145 150 155 160  
187 Ala Ala Ser Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu Arg Ala  
188 165 170 175  
189 Ala Leu Ala Ser Val Gly His Leu Tyr Gly Pro Tyr Gly Lys Glu Leu  
190 180 185 190  
191 Pro Ala Met Gly Ser Pro Leu Ser Pro Leu Pro Asn Ala Leu Pro Pro  
192 195 200 205  
193 Ala Leu His Gly Ala Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro  
194 210 215 220  
195 Leu Ala Ala Tyr Gly Pro Pro Gly His Leu Ala Gly Asp Lys Leu Leu  
196 225 230 235 240  
197 Pro Pro Ala Ala Phe Glu Pro His Ala Ala Leu Leu Gly Arg Ala Glu  
198 245 250 255  
199 Asp Ala Leu Ala Arg Gly Leu Pro Gly Gly Gly Gly Thr Gly Ser  
200 260 265 270  
201 Gly Gly Ala Gly Ser Gly Ser Ala Ala Gly Leu Leu Ala Pro Leu Gly  
202 275 280 285  
203 Gly Leu Ala Ala Ala Gly Ala His Gly Pro His Gly Gly Gly Gly  
204 290 295 300  
205 Pro Gly Gly Ser Gly Gly Pro Ser Ala Gly Ala Ala Ala Glu Glu  
206 305 310 315 320  
207 Ile Asn Thr Lys Glu Val Ala Gln Arg Ile Thr Ala Glu Leu Lys Arg  
208 325 330 335  
209 Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Ile Leu Cys Arg Ser  
210 340 345 350  
211 Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro Trp Ser Lys  
212 355 360 365

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213 Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys Trp Leu Gln  
214 370 375 380  
215 Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala Ala Cys Lys  
216 385 390 395 400  
217 Arg Lys Glu Gln Glu Gln Gln Lys Glu Arg Ala Leu Gln Pro Lys Lys  
218 405 410 415  
219 Gln Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu Ile Ala Ile  
220 420 425 430  
221 Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Val Thr Ile Ser  
222 435 440 445  
223 Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn  
224 450 455 460  
225 Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala  
226 465 470 475 480  
227 Pro Gly Gly Pro Ala Gly Ala Thr Ala Thr Phe Ser Lys Ala  
228 485 490

**VERIFICATION SUMMARY**

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